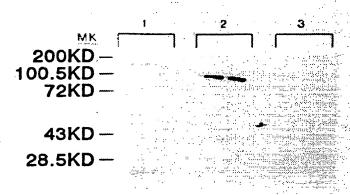
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FIGURE 1



1 - anti- EGFr PoAB RK-2 2 - Cyt-356 MoAB/RAM 3 - RAM WO 94/09820 PCT/US93/10624

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FIGURE 2A

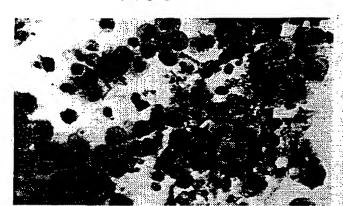


FIGURE 2B

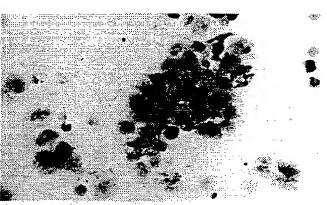


FIGURE 2C

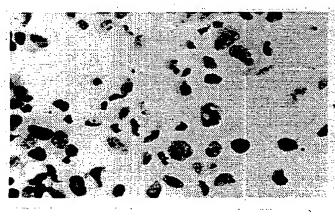
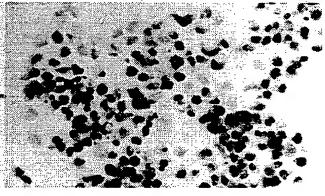


FIGURE 2D



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FIGURE 3A

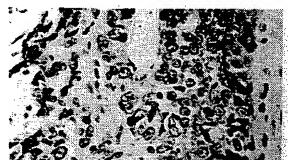


FIGURE 3B

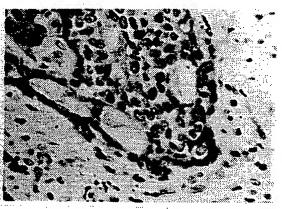


FIGURE 3C

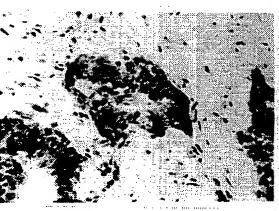
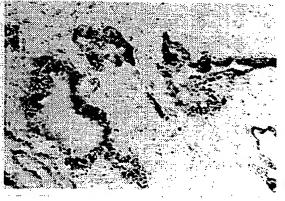


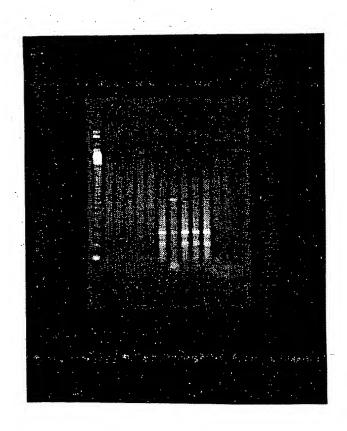
FIGURE 3D



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FIGURE 4

5/48 FIGURE 5

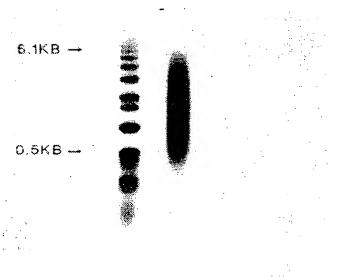


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⁰⁸/466381

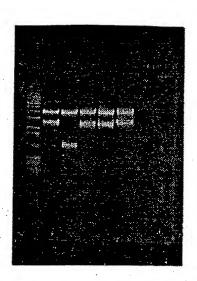
7/48

FIGURE 7

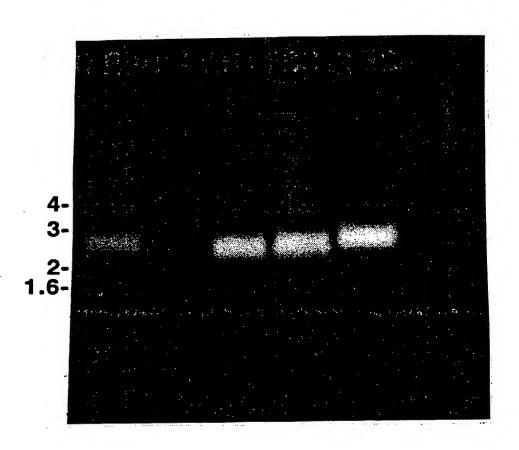


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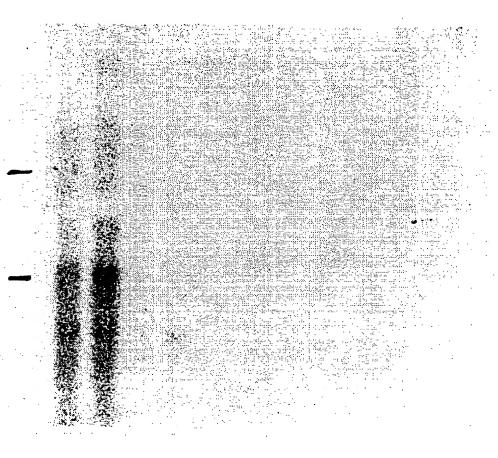
FIGURE 8



9/48 FIGURE 9



10/48 FIGURE 10

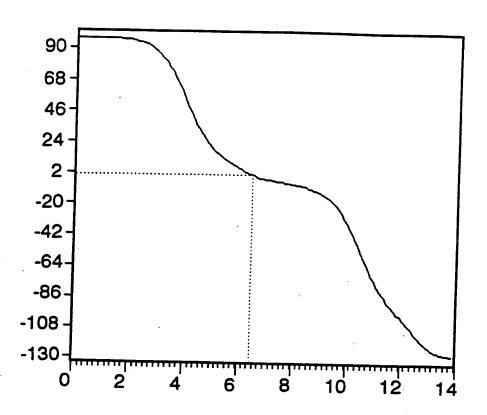


11/48 FIGURE 11

12/48

FIGURE 12B

13/48 FIGURE 13



ſВ

FIGURE 14-1

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codes. Sequence shown with conformation

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are given conformation Ø in residues more or S of stretch Consecutive overlined.

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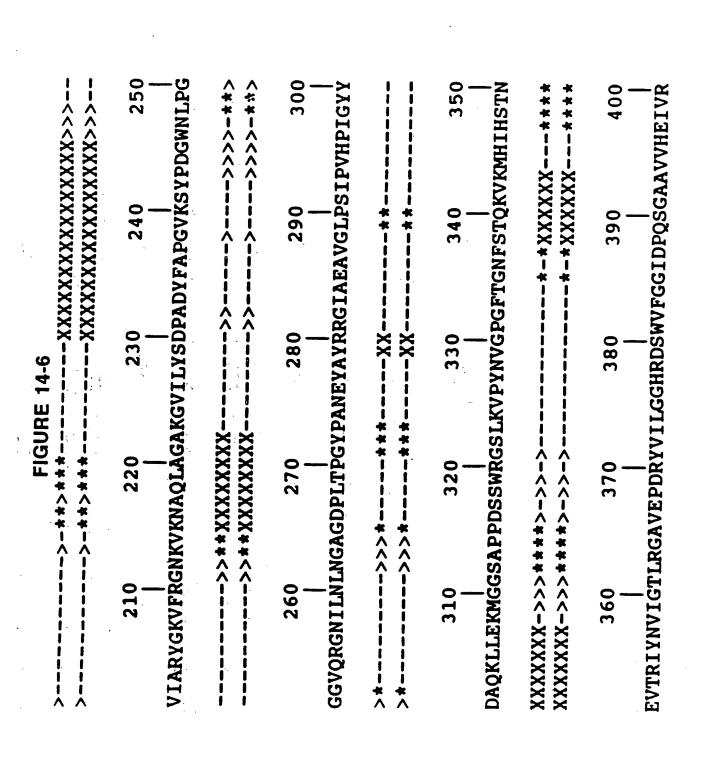
FIGURE 14-4

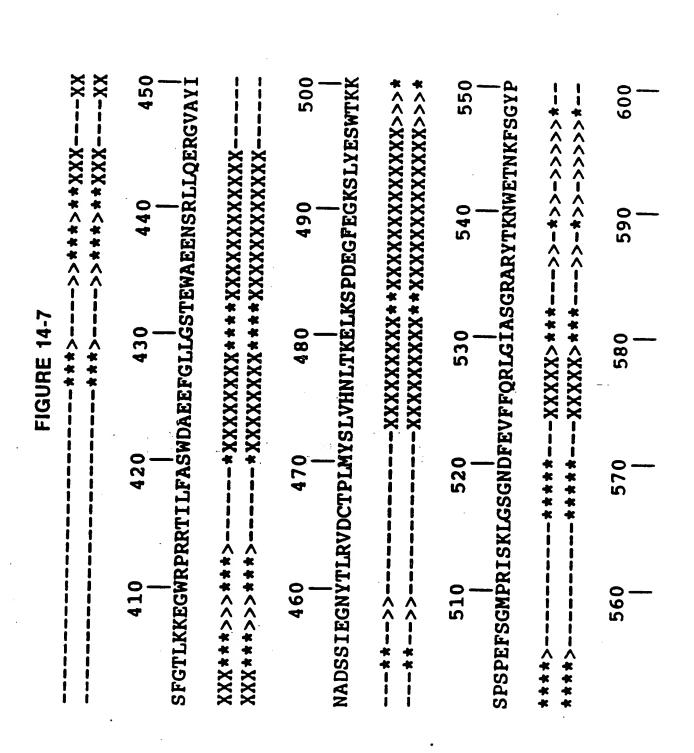
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**************************************	110 120 130 140 150 150 150 KEFGLDSVELAHYDVLLSYPNKTHPNYISIINEDGNEIFNTSLFEPPPPG	<pre><<*****<<x***<*< th=""><th>160 170 180 190 200 XENVSDIVPPFSAFSPQGMPEGDLVYVNYARTEDFFKLERDMKINCSGKI</th></x***<*<></pre>	160 170 180 190 200 XENVSDIVPPFSAFSPQGMPEGDLVYVNYARTEDFFKLERDMKINCSGKI
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LYHSVYETYELVEKFYDPMFKYHLTVAQVRGGMVFELANS I VLPFDCRDY	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	610 620 630 640 650 	**************************************	660 670 680 690 700 QDFDKSNPIVLRMMNDQLMCLERAFIDPLGLPDRPFYRHVIYAPSSHNKY	XXXXXXXXXXXXX>>+++>	710 720 730 740 750 	XXXXXXXXXXXXXXXXXXX****XXXXXXXX
ETYELVEKFYDPMFK	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	610 620 XADKIYSISMKHPQE		660 670 NPIVLRMMNDQLMCI		710 720 GIYDALFDIESKVDF	****XXXXXXXX<
LYHSVY		AWLRK	-XXXXXXXXXXX	QDFDKS	XX >> >	AGESFP	

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22/48 FIGURE 15A

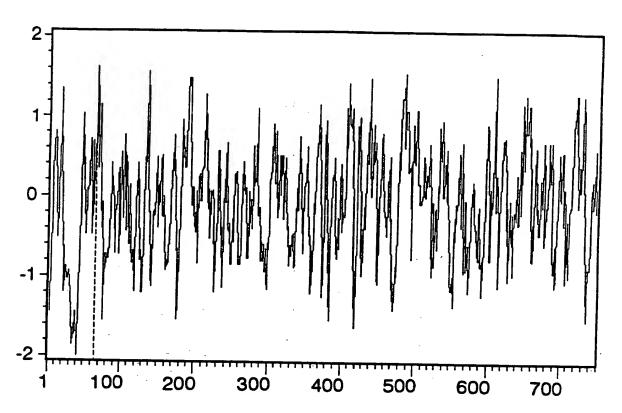


FIGURE 15B

Done on sequence PMSANTIGEN. Total number of residues is: 750.

Analysis done on the complete sequence.

-> This is the value recommended by the authors The averaging group length is: 6 amino acids. The method used is that of Hopp and Woods.

The three highest points of hydrophilicity are:

Asp-Glu-Leu-Lys-Ala-Glu Asn-Glu-Asp-Gly-Asn-Glu Lys-Ser-Pro-Asp-Glu-Gly **68** 137 487 to 132 482 From From Fron 1.62 1.57 1.55

Ah stands for: Average hydrophilicity.

Note that, on a group of control proteins, only the highest point was in 100% of the cases assigned to a known antigenic group. The second and third point: gave a proportion of 33% of incorrect predictions.

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opt	321	311	266	321	A	Ē.	AT::	D & 0
initl	120	164	145	120	70 CCAGGTT	ccAGGCT 1040	30 CCAAGTAT :: :: CCCCACAT 1100	90 SGTGGCTC : :: SATGGAGA
initn	203		145	203	1070 TCACACC	ACACC	1130 GGTCTTCC/ :: :: :: GGACTACC/	1190 AAAATGGGTGG :::::::: AAAATGGATGG
FIGURE 16-1	G.dall	Rat transferrin receptor mRNA, 3' end.	Human transferr	R G.gallus mRNA for transferrin receptor % identity in 717 nt overlap	1020 1030 1040 1050 1060 1070 TGTCCAGCGTGGAATATCCTAAATCTGAATGGTGCAGGAGACCCTCTCACACCAGGTTA	TACACTTATCCCATTCGGACATGCCCACCTTGGAGCCCCTTACACCCCAGGCTT 990 1000 1010 1020 1030 1040	1080 1090 1100 1110 1120 CCCAGCAAATGAATATGCTTATAGGCGTGGAATTGCAGAGGCTGTT ::::::::::::::::::::::::::::::::	1140 1150 1160 1170 1180 TCCTGTTCATCCAATTGGATACTATGATGCACAGAAGCTCCTAGAA :::::::::::::::::::::::::::::::::
mbo bost	THE DES	RATTRER	HUMTERR	CHKTFER 51.9%	pmsgen	CHKTFE	pmsgen CHKTFE	pmsgen

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CTGG AA 1210	AGT :: AGA	rgt ::: rgt	AGC * :
10 1220 1230 1240 1250 TAGCAGCTGGAGGAAGTCTCAAAGTGCCCTACAATGTTGGACCTGG :: :::::::::::::::::::::::::::::::::	70	60 1370 GGAACCAGACAGATATG ::::::::::: AGAACCTGATCGGTATG 310 1320	1400 1410 1420 1430 CACCGGGACTCATGGTGTTTTGGTGGTGGAGTGGAGT ::::::::::::::::::::::::::::::::::::
1250 TGTTGG ::::	1310 CACTCTACCAA :: ::: AACAATTCCAT 50 126	1370 :AGACAG :: : :TGATCG	1430 TCAGAG: : : : TGGCAC
1240 1 CCCTACAATGT ::: :: :: FCCTGTAAGGT	OCACTC :: AACAA	360 TGGAACC :::: AAGAACC	0 GACCC : : AAAGC 70
1240 rgcccr ::: -TTCCT	1300 CACATCCA : : : SATGTGAA 1250	1360 CAGTGG : : FTGAAG	1420 STATTGA : : FGGCTAA 1370
AAAG	ATGCZ : CTAGZ	O AGGAG(::: GGGATT	GGTG(:::: GGAGJ
1230 GTCTC :: CGATC 1190	0 1290 AAAAAGTCAAGATG(:: :: : FAATGGTGAAACTA(30 1240	1350 TCAGAG :: : TCCAGG	1410 rgtttg : scccag 1360
123 AGGAAGTCT ::: AGGTGCGAT	AAAAG :: : AATGG 0	340 13 AGGTACTCTCA ::: :: :: CGGTGCTATCC	ATGGG
1220 GCTGGAGAGG : ::: ::: GTTGGAAAGG	1280 ACACAA : : : AGA-TA	1340 NTAGGT : ::: TCGGT 1290	1400 CGGGACTCA : :::: AGAGACTCC 1350
SCAGC	TTCTV	TGTGA : CATCI	ccess : : sagas
1210 GATAC :: :: GA-AG	1270 AACTT : GA	1330 TACAA :: CTGAA 1280	1390 GGTCA(: :: GCCCA(
CACCA : GCTCT	CTGGA : ::: :2AGGA 1220	BATT.	TGGGAG : :::: TTGGAG
1200 1210 1220 1230 1240 1250 AGCACCACCAGATAGCAGCTGGAGGAAGTCTCAAAAGTGCCCTACAATGTTGGACCTGG :: :::::::::::::::::::::::::::::::::	1260 12 CTTTACTGGAAA(: ::: : CAAAGCAGGAGA- 1220	1320 1330 1340 1350 1360 1370 GACAAGAATTTACAATGTGATAGGTACTCTCAGAGGAGCAGTGGAACCAGACAGA	1380 1390 1400 1410 1420 1430 CATTCTGGGAGTCACCGGGACTCATGGGTGTTTTGACCCTCAGAGTGGAGC : :::: ::: :::::::::::::::::::::::::
pmsgen	pmsgen CHKTFE	pmsgen CHKTFE	pmsgen CHKTFE
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FIGURE 16-3

⁰⁸/466381

CHKTFE

	26/4	48	
1440 1450 1460 1470 1480 1490 AGCTGTTCATGAAATTGTGAG——GAGCTTTGGAACACTGAAAAGGAAGGGTGGAG :::::::::::::::::::::		pmsgen TACTGAGTGGGCAGAGAATTCAAGACTCCTTCAAGAGCGTGGCGTGGCTTATATTAA :::::::::::::::::::::::::::::	1620 1630 1640 1650 1660 1670 pmsgen TGC-TGACTCTATAGAAGGAAACTA-CACTCTGAGAGTTGATTGTACACCGCTGATG
1470	1540 GAAGAATTTGC : : : : : : : : : : : : : : : : : : :	1600 GAGCGTGGCG7 : : : : : : : : : : : : : : : : : : :	1650 1660 GAGAGTTGATTGTA
1470 GAGCTTTGGA :::::: STGATCTCAGAC 1420	1520 1530 1540 TGTTTGCAAGCTGGATGCAGAATTTTGG : X::::::::::::::::::::::::::::::::::	30 1590 AGACTCCTTCAA : : :: 3CCATGCTGCAT 1540	1640 16 ACTA-CACTCTGA
1460 ************************************	510	570 1580 AGGAGAATTCAAG :::::X AGGGGTACTCTGC	1630 1
1440 1450 AGCTGTTGTTCATGA :::::::::::::::::::::::::::::::::::	1500 15 ACCTAGAAGAACAAT ::::::::::: ACCGAGGCGAAGCAT 1450 1460	1560 15 FACTGAGTGGGCAGA :::::::::::::::::::::::::::::::::::	1620 TGACTCATCTA
pmsgen AGCTG ::: CHKTFE TGCTA	1500 1 pmsgen ACCTAGAAGAACAA :::::::::::::::::::::::::::::	pmsgen TACTG::::CHKTFE TACTG	msgen TGC-
H O	H 0	11)

1680 TACAGCTTGGTACA(:: : :	FE TATATGCTGCTGAGTATTATGAGGGGGTGAAGAATCCAGCAGCAGTCTCAGAGAGC 1630 1640 1650 1660 1670 1680	1740 1750 1760 1770 1780 1790 pmsgen AAATCTCTTTATGAAAGTTGGACTAAAAAAGTCCTTCCCCAGAGTTCAGTGGCATGCCC ::::::::::::::::::::::::::::::::::	FECTCTATAACAGACTTGGCCCAGACTGGGTAAAAGCAGTTGTTCCTCTTGGCCTGGA
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1GURE 16-5

311	- C) I	\CT
164	TGGCT	rragari	.0 \ATG
164	1210 1230 1240 1250 1250 pmsgen ccaccagargergagagagagagagagagagagagagagagagag	RATTRF TGCAGAAAACTATTCAAAAACATGGAAACTGTCCTCCTAGTTGGAATATAGATTC 610 620 630 640 650 650	1260 1270 1280 1290 1300 1310 pmsgen -TACTGGAAACTTTTCTACACAAAAAGTCAAGATGCACATC-CACTCT-ACCAATG RATTRF CTCATGTAAGCTGGAACTTTCACAGAATCAAAATGTGAAGCTCACTGTGAACAATGTAACT 670 680 690 700 710
, 3' end.	1240 AGTGCCCTAC	ACTGTCCTCC 650	1300 ATGCACATC-CAC ::: :::
Rat transferrin receptor mRNA, 3' end. lentity in 560 nt overlap	1230 GAAGTCTCAA	atggaaggaa 640	AAAAGTCAAG
TTRFR Rat transferrin receptor 55.5% identity in 560 nt overlap	1220 AGCTGGAGAG	ATTCAAAAAC 630	1280 TTTCTACACA :: GGAACTTTCA 690
Rat trans dentity in	1210 ACCAGATAGC	CAGAAAAGCT 620	1270 ACTGGAAACT :::::: CATGTAAGCT
RATTRFR 55.5% 1			•
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pmsgen --AAGTGACAAGAATTTACAATGTGATAGGTACTCTCAGAGGAGCAGTGGAACCAGACAG

1360

1350

1340

1330

1320

FIGURE 16-6

RATTRF GAAAGAAACAAGAATACTTAACATCTTTGGCGTTATTAAAGGCTATGAGGAACCAGACCG

740

1390

1380

780

29/	48	08/466381
CCTCAGAG ::::	1480 -AAAAGGAA ::: :: TCAAAAGAT 00	1540 TTTGGTCTT : :: : TATGGAGCT 60
GTATTGAC::::::-GTTGCGAA	14. A-CTGAA. S:: ATATGATTTC.	30 15 CAGAAGAATT ::::::: CAGGAGACTA 960
TGTTTGGTGGTA :::::: GCCCTGGT-GTT	1470 TTTGGAACA :: : : : ATTCTCAGA	1530 CTGGGATGCA :::: :::: CTGGACTGCA 950
PMSGEN ATATGTCATTCTGGGAGGTCACCGGGACTCATGGGTGTTTGGTGGTATTGACCCTCAGAG :: : : : : : : : : : : : : : : : : :	1440 1450 1460 1470 1480 pmsgen T-GGAGCTGTTGTTGAAATTGTGAGGAGCTTTGGAACA-CTGAAAAAGGAA : :::::::::::::::::::::::::::::	1490 1500 1510 1520 1530 1540 pmsgen GGGTGGAGCCTAGAACAATTTTGTTTGCAAGCTGGGATGCAGAAGAATTTGGTCTT :::X:::::::::::::::::::::::::::::::
AGGTCACCGG:: : : : AGCCCCAGAGA	1450 FTCATGAAATT : ::::: CTGTTGAAACT 870	1510 AGAACAATTT :::::: AGGAGTATTA 930
CATTCTGGGAG CATTCTGGGAG TGTAGTAGGAG	1440 GGAGCAGCTGTTG1 ::::::::::: GGGAACAGGTCTT-(1490 GGTGGAGACCTAGAAGA :::X:::::::::::::::::::::::::::::::::
n ATATGT :: : F CTACAT	T-GGAG ::: TGGGAA 850	1490 :::: : GGATTT 910
pmsgei RATTRI	pmsgen RATTRF	pmsgen Rattr

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RATTRF CCCCCTATTATACACTTATGGGGAAGATAATGCAGGA-1100 1110 1120

	1550	1560	1570	1580	1590 1690	1600 1600
s pmsgen		TACTGAGTGGG	CAGAGGAGAA-	I'I'CAAGACI	CTTGGTTCTACTGAGTGGGCAGAGGAGAATTCAAGACTCCTTCAAGAGCGTGGCGTG	9 T 9 7 9
JBS	••	•••	×			•• [
E RATTRE	F GTTGGTCC	GACTGAGTGGC	TGGAGGGGTAC	CTTTCATCTTT	GTTGGTCCGACTGAGTGGCTGGAGGGGTACCTTTCATCTTTGCATCTTAAAGGCTTTTC	CITIC
	970	086	990 10	1000 10	1010 1020	0
SHEE	1610	1620	1630	1640	1650	1660
magen	GCTTATAT	TAATGCTGACT	CATCTATAGAA	3GAAACTA-CA	GCTTATATTATGCTGACTCATCTATAGAAGGAAACTA-CACTCTGAGAGTTGATTGTAC	TGTAC
	•••	•••	••	•••	•••	••
	ACTTACATI	FAAT-CTGGAT?	AAAGTCGTCCT (SGGTACTAGCA	RATTRF ACTTACATTAAT-CTGGATAAAGTCGTCCTGGGTACTAGCAACTTCAAGGTTTCTGCCAG	GCCAG
	1030	1040	1050	1060	1070 1080	80
			,	1	,	0
	1670	1680	069T	7 / 00	1/10	1/20
pmsgen	pmsgen ACCGCTGATGTAC	GTACAGCTTGG	TACACAACCT	ACAAAAGAGC	AGCTTGGTACACCTAACAAAAGAGCTGAAAAGC-CCTGATGAAG	TGAAG
ı		•				

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pmsgen GCTTTGAAGGCAAATCTCTTTAT-GAAAGTTGGACTAAAAAAAGTCCTTCCCCAG	Ilearceanarial Cialai Ceanacachta a canacachta 1140 1150 1160 1170 1180 1190	1780 1790 1800 1810 1820 1830 pmsgen AGTTCAGTGCCAGGATAAGCAAATTGGGATCTGGAAATGATTTTGAGGTGTTCT	CATTCCCTTTTCTTGCATATTCAGGAATCCCAGCAGTTTCTTTC
1750 1760 AGTTGGACTAAAAAAAGTC	1180	1820 GAAATGATTT	GAATCCCAGC 1240
1750 AGTTGGA : ::::	1170	1810 ATTGGGATCTG	GCATATTCAG 1230
1740 TCTTTAT-GAA	1160 1160	1800 GATAAGCAAA	CCCTTTTCTT 1220
SGCAAATCTCTT	1150	1790 GCATGCCCAG	ATGCTGCATT 1210
		1780 AGTTCAGTG	RATTRF CCTTGGACAATGCTG
·	KATTKF		
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	<u>.</u> د ر	ည		K	0.0 B. A
	CTACA	AACCI	1320 1330 AAGTGACAAGAATTTACAA ::::::::::::::::::::::::::::::	1380 ATATGTCATTCTGGGAGGTC2 ::::::::::::::::::::::::::::::::::::	1450 TTCATG : TATTGA
C	CTTTT	rggri	1320 13 AAGTGACAAGAATTTA ::::::::: AAGAGATAAAAATTCT 0 1250	TGGG1 : :: TTGGC	0 1430 1440 GACCCTCAGAGT-GGAGCAGCTGTTGT : : : : : : : : : : : : : : : : : : :
1270	AAAC	AGGATG 1190	1320 GACAAGA ::::: GATAAAA 1250	1380 CATTCTG : : TGTAGTT 1310	1440 AGCT(:::AGCT()
	-TGG	ATGT	AGTG	TGTC:::TGTT	GAGC:::::GCAC
1260	ACCTGGCTTTAC-TGGAA	CTAC	AAG ::: :TGAAAG	0 GATA:::ACTA:	0 GT-GG ::::: GTAGG
12	GGCI	GACT	9: ::: :::::::::::::::::::::::::::::	1370 GACAGA :: GATCAC	1430 CAGAG
	SACCT	AAAACA 1170	1310 ACCAAT : ::: AGCAAT	0 GAACCA ::::: GAACCA 1290	0 GACCCT : : AAATC- 1350
1250	GTTG	TGGAA	1300 1310 ATC-CACTCT-ACCAATG ::::::: AGCTCACTGTGAGCAATG 1220 1230	1360 1370 GTGGAACCAGACAG :::::::: GTAGAACCAGATCA 1290 1	1420 ATTGA GCAA
	CAAT	TGAC 0	CACT	AGCA CTTT	O 1 TGGTGGTA ::::::
240	CCTA	CCTCT 1160	1300 ATC-CP	50 GAGGAC ::: AAGGCT	10 TTGGT ::: CCTGGA 1340
	GTG	TGTC	ATGCAC::: ATGTGA	TCTCA:	14. SGTGT
30	rcaa.	GAGA(1150	1290 CAAGAT : :: AAGAAT	0 GTACT : GAGTT 1270	00 FCATGGG ::::: 3CATGGG
1230	AGTC	GAAG	AGTCZ	1340 ATAGG : :: TTTGG	1400 GGGACTC : :: : GAGATGC
	AGGA	R TATG	280 n AAAAAGT : ::: R AGAAAGC	1340 1350 1360 1370 1380 1390 n TGTGATAGGTACTCTCGGAGGAGCAGTGGAACCAGACAGA	n CCGG(: R GAGA(1320
	pmsgen AGGAAGTCTCAAAGTGCCCTACAATGTTGGACCTGGCTTTAC-TGGAAACTTTTCTACAC	HUMTFR TATGGAAGGACTGTCCCTCTGACTGGAAAACAGACTCTACATGTAGGATGGTAACCTC	1280 1290 1300 1310 1320 1330 pmsgen AAAAAGTCAAGATGCACATC-CACTCT-ACCAATGAAGTGACAAGAATTTACAA ::::::::::::::::::::::::::::::	1340 1350 1360 1370 1380 1390 pmsgen TGTGATACTCTCAGAGGAGCAGTGGAACCAGACAGATATGTCATTCTGGGAGGTCA : :::::::::::::::::::::::::::::::::::	1400 1410 1430 1440 1450 pmsgen CCGGGACTCATGGTGTATTGACCCTCAGAGT-GGAGCAGCTGTTGTTCATG ::::::::::::::::::::::::::::::::::::
	Smd	HOL	pms HUM	MOH	PMS

FIGURE 16-1

1460
pmsgen 7 HUMTER 7 15 14 HUMTER 7 15 HUMTER 8 HUMTER 6 HUMTER 6

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FIGURE 16-11

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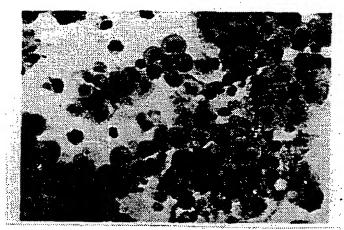


FIGURE 17B

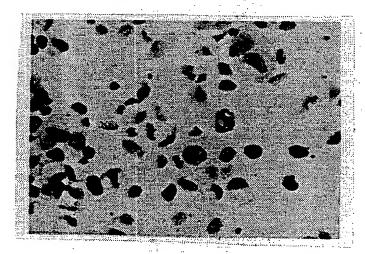
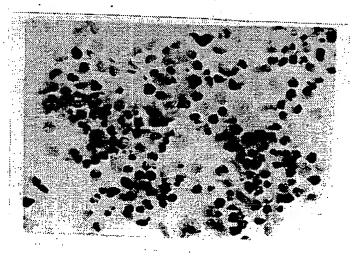


FIGURE 17C



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FIGURE 18

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FIGURE 19

1 2 3 4

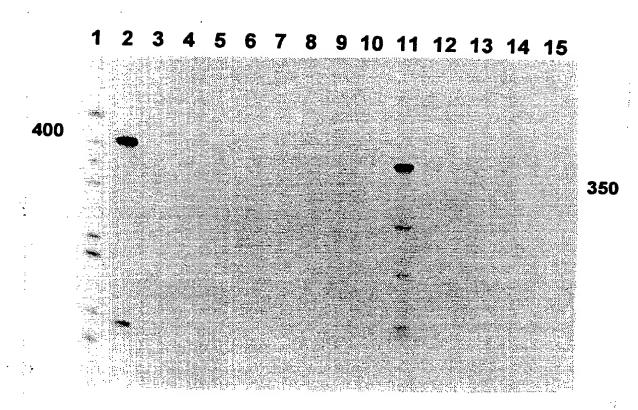
200 kDa ---

100 kDa ---

69 kDa ----

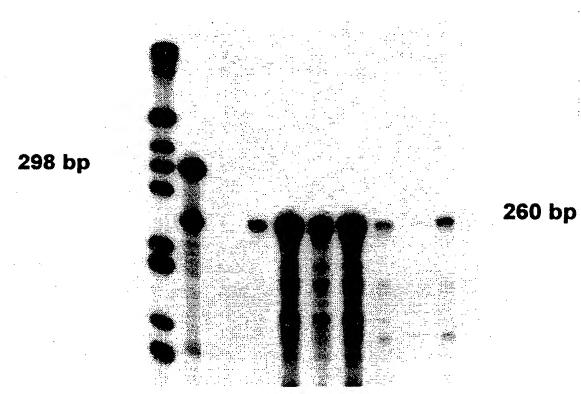
- PSM

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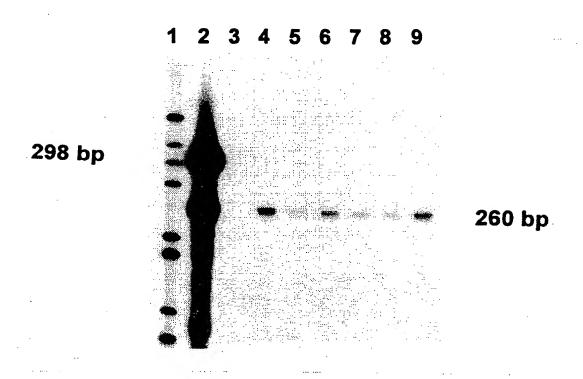


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1 2 3 4 5 6 7 8 9 10



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CELL LINE/TYPE	11p11.2-13 REGION	METASTATIC	PSM RNA DETECTED	PSM DNA DETECTED
LNCap			++	ND
HUMAN PROSTATE			++	ND
A9 (FIBROSARCOMA)	NO	NO	_	-
A9(11) (A9+HUM. 11)	YES	NO	-	REPEAT
AT6.1 (RAT PROSTATE)	NO	YES		-
AT6.1-11-c11	YES	NO	+	++
AT6.1-11-c12	NO	YES	-	-
R1564 (RAT MAMMARY)	NO	YES	_	-
R1564-11-c14	YES	YES	_	+
R1564-11-c15	YES	YES	_	REPEAT
R1564-11-c16	YES	YES	_	ND
R1564-11-c12	YES.	YES	ND	+

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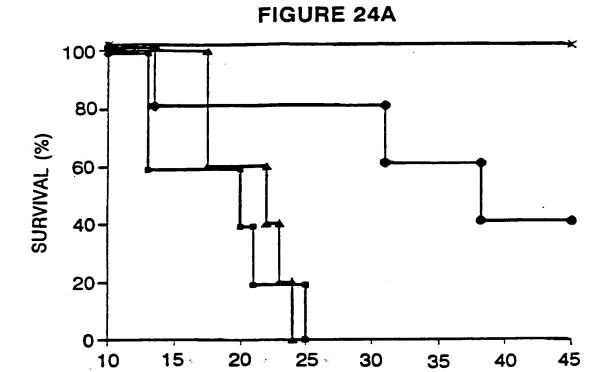


FIGURE 24B

TIME (DAYS)

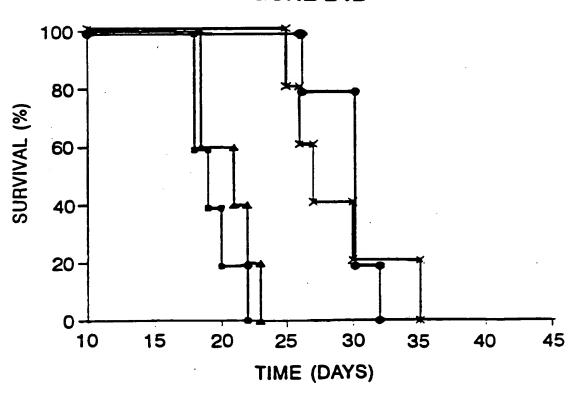
25 -

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FIGURE 25A

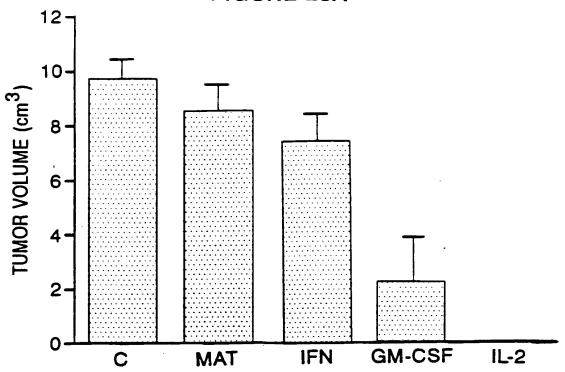
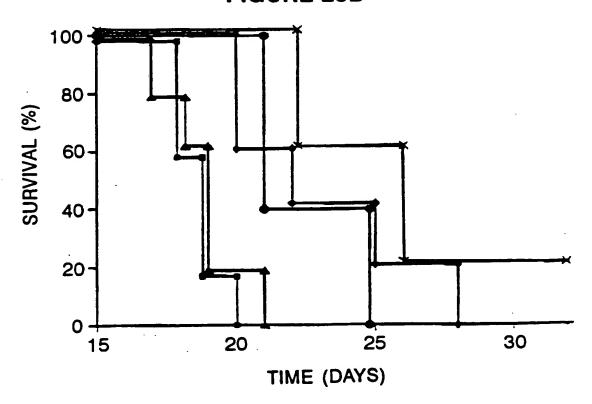
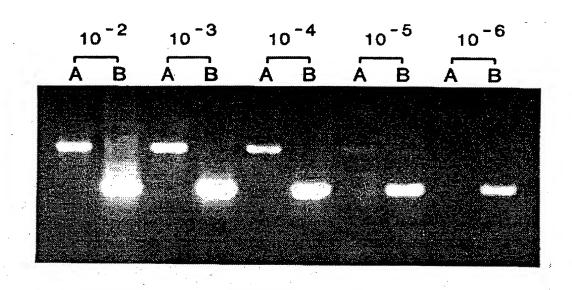


FIGURE 25B



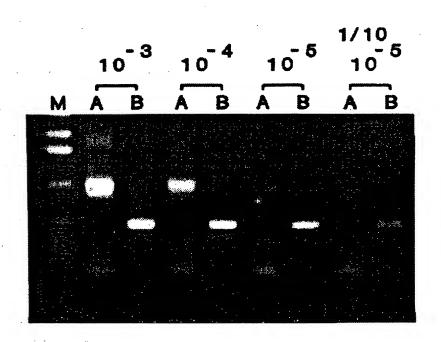
SUBSTITUTE SHEET (RULE 26)

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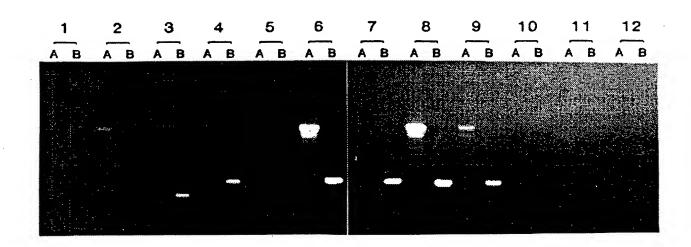


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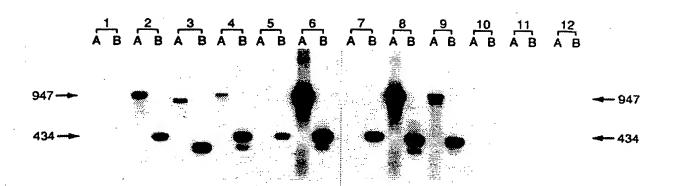


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		I Idone	30				
Patient	Stage	Treatment	PSA	PAP	PSA-PCR	PSM-PCR	
1	T2NxMo	None	8.9	0.7	_	+	
2	T2NoMo	RRP 7/93	6.1	-	-	+	
3	T2CNoMo	PLND 5/93	4.5	0.1	_	+	
4	T2BNoMo	RRP 3/92	NMA	0.4	-	+	
5	T3NxMo	Proscar + Flutamide	51.3	1.0	_	+	
6	Recur T3	I-125 1986	54.7	1.4	-	+	
7	T3ANoMo	RRP 10/92	NMA	0.3	_	+	
8	T3NxMo	XRT 1987	7.5	0.1		-	
9	T3NxMo	Proscar + Flutamide	35.4	0.7	-	-	
10	D2	S/P XRT Flutamide +Emcyt	311	4.5	`+	+	
11	D2	RRP 4/91 Lupron 10/92 Velban + Emcyt 12/92	1534	1.4	· +	+	
12	T2NoMo	RRP 8/91	NMA	0.5	_	+	
13	ТЗМоМо	RRP 1/88 Lupron + Flutamide 5/92	0.1	0.3	-	-	
14	D1	PLND 1989 XRT 1989	1.6	0.4	-	-	
15	D1	Proscar + Flutamide	20.8	0.5	-	-	
16	T2CNoMo	RRP 4/92	0.1	0.3	_	-	
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